			1111122222	222222222	2222233333	333333333	3333344444
	3444444556	6666666679	0333400468	888888999	9999900000	0011112233	3333414555
	7345667351	2256788809	6669424121	1378899012	5667744456	6755573711	1167394189
	3265476314	0398403958	8035356281	7511567432	9271637842	6303671735	6779204087
PMEN3	CCTAAACCAC	TTTGCGACAA	AGACGCAATC	TCGGAACTGT	TGTAAAACGT	CTGCCTCTGG	TTGTGTTAAC
9A/1			.CGTATGGCT	CTAACGACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
9V/5			.CGTA-GGCT	CTAAC.ACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
9V/6			.CGTATGGCT	CTAAC.ACTC	CACTGGCAAC	TCATTCTCAA	AATCACCGGT
PMEN1	TTCTGGAAGT	GACATATTGG	G				
			1				
	455555555	555555555	5555666666	666666666	677777777	777777777	7788888899
	8233444457	7788889999	9999113344	4445559999	9000000011	1111111222	2215888923
	8233444457 7556235985	7788889999 7902771234	9999113344 5569172334	4445559999 4480032388	9000000011 9011223324	11111111222 4467778134	2215888923 4655699347
	020011110,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	000011				2210000020
PMEN3	7556235985	7902771234	5569172334 3760086510	4480032388 3681337647	9011223324 9824692350	4467778134	4655699347 5870639581
PMEN3 9A/1	7556235985 3640074361 TTGTACGTTT	7902771234 8383486903	5569172334 3760086510 CGTCCTATAC	4480032388 3681337647	9011223324 9824692350	4467778134 3640392932	4655699347 5870639581
	7556235985 3640074361 TTGTACGTTT	7902771234 8383486903 GGTTAAAGCA	5569172334 3760086510 CGTCCTATAC	4480032388 3681337647 ATTGATTAAA	9011223324 9824692350 CTTAATCATC	4467778134 3640392932 ACGTTAGGCA	4655699347 5870639581 AAGCGATGGC
9A/1	7556235985 3640074361 TTGTACGTTT CCACGTAGCC	7902771234 8383486903 GGTTAAAGCA AACGCCGAGC AACGCCGAGC	5569172334 3760086510 CGTCCTATAC ATCATCCCTT	4480032388 3681337647 ATTGATTAAA TCGATCCCTT	9011223324 9824692350 CTTAATCATC TCCCTCACGT	4467778134 3640392932 ACGTTAGGCA GAACCTAATT	4655699347 5870639581 AAGCGATGGC GGT
9A/1 9V/5	7556235985 3640074361 TTGTACGTTT CCACGTAGCC CCACGTAGCC	7902771234 8383486903 GGTTAAAGCA AACGCCGAGC AACGCCGAGC	5569172334 3760086510 CGTCCTATAC ATCATCCCTT ATCATCCCTT	4480032388 3681337647 ATTGATTAAA TCGATCCCTT TCGATCCCTT	9011223324 9824692350 CTTAATCATC TCCCTCACGT TCCCTCACGT	4467778134 3640392932 ACGTTAGGCA GAACCTAATT GAACCTAATT	4655699347 5870639581 AAGCGATGGC GGT

Figure S3. Variable site output showing the PMEN3 putative import region 4 and flanking regions. Regions from the genomes of the PMEN1 reference strain, the PMEN3 reference strain and the PMEN3 ancestral representatives, 9A/1, 9V/5 and 9V/6 are shown. Numbers indicate variable site positions within the alignment. Periods (".") indicate bases identical to the PMEN3 reference at a given site. Dashes ("-") indicate missing bases at a given site. Red brackets indicate the putative imported region.